What is claimed is:

1. An isolated Ikaros transcriptional control region comprising one or more Ikaros regulatory element.

2. The Ikaros transcriptional control region of claim 1, comprising all or a functional fragment of a promoter of the β cluster.

3. The Ikaros regulatory control region of claim 1, comprising all or a functional fragment of a promoter of the γ cluster.

4. The Ikaros regulatory control region of claim 2, further comprising all or a functional fragment of a promoter of the γ cluster.

5. The Ikaros regulatory control region of any of claims 2, 3 or 4, further comprising one or more Ikaros regulatory element from the α cluster, the ε cluster, the η cluster or the θ cluster.

6. The Ikaros regulatory control region of claim 4, further comprising the ε cluster or a portion thereof.

7. A DNA construct comprising an Ikaros transcriptional control region of claim 1 and a sequence encoding a reporter molecule.

8. The DNA construct of claim 7, wherein the reporter molecule is a reporter molecule which can luminesce or fluoresce.

9. The DNA construct of claim 7, wherein the reporter molecule is selected from a beta-galactosidase gene, a luciferase gene, a green fluorescent protein gene, an alkaline phosphatase gene, a horseradish peroxidase gene, and a chloramphenicol acetyl transferase gene.

10. The DNA construct of claim 7, wherein the reporter molecule is green fluorescent protein.

11. A transgenic animal, or cell or tissue therefrom, comprising a transgene includes an Ikaros transcriptional control region operably linked to a sequence which is functionally unrelated to the Ikaros gene.

12. The transgenic animal of claim 11, wherein the animal is a rodent.

13. The transgenic animal of claim 12, wherein the rodent is a mouse.

14. The transgenic animal of claim 11, wherein the Ikaros transcriptional control region includes one or more Ikaros regulatory element.

15. The transgenic animal of claim 11, wherein the Ikaros transcriptional control region comprises the β cluster or a functional fragment of the promoter of the β cluster.

16. The transgenic animal of claim 11, wherein the Ikaros transcriptional control region comprises the γ cluster or a functional fragment of the promoter of the γ cluster.

17. The transgenic animal of claim 15, wherein the Ikaros transcriptional control region further comprises the γ cluster or a functional fragment of the promoter of the γ cluster.

18. The transgenic animal of any of claims 14, 15, or 16, wherein the Ikaros transcriptional control region further comprises one or more Ikaros regulatory element from the α cluster or a portion thereof, the ε cluster or a portion thereof, the η cluster or a portion thereof, or the θ cluster or a portion thereof.

19. The transgenic animal of claim 15, wherein the Ikaros transcriptional control region further comprises the ε cluster or a portion thereof.

20. The transgenic animal of claim 19, wherein the Ikaros transcriptional control region comprises a portion of the ε cluster.

21. The transgenic animal of claim 11, wherein the sequence functionally unrelated to the Ikaros gene encodes a reporter molecule.

22. The transgenic animal of claim 21, wherein the reporter molecule is a reporter molecule which can luminesce or fluoresce.

23. The transgenic animal of claim 21, wherein the sequence encoding the reporter molecule is selected from a beta-galactosidase gene, a luciferase gene, a green fluorescent protein gene, an alkaline phosphatase gene, a horseradish peroxidase gene, and a chloramphenicol acetyl transferase gene.

24. The transgenic animal of claim 21, wherein the reporter molecule is green fluorescent protein or a variant thereof.

25. The transgenic animal of claim 24, wherein the reporter molecule is a variant of green fluorescent protein.

26. The transgenic animal of claim 25, wherein the variant of green fluorescent protein is selected from the group consisting of EGFP, EBFP, EYFP, d2EGFP, ECFP, and GFPuv.

27. The transgenic animal of claim 11, wherein the genome of the animal further comprises an alteration by disrupting at least one exon of the endogenous Ikaros gene.

28. The transgenic animal of claim 27, wherein the endogenous Ikaros gene is disrupted by insertion of a nucleic acid sequence.

29. The transgenic animal of claim 28, wherein the insertion results in any of an inversion, deletion, translocation, or reciprocal translocation.

30. The transgenic animal of claim 28, wherein the insertion is in or alters the sequence, expression, or splicing of one or more of the following exons: exon 1/2, exon 3, exon 4, exon 5, exon 6, and exon 7.

31. The transgenic animal of claim 28, wherein the insertion is in or alters the sequence, expression, or splicing of a DNA binding domain of the Ikaros gene.

32. The transgenic animal of claim 28, wherein the insertion results in a deletion of portions of exon 3 and exon 4.

33. The transgenic animal of claim 28, wherein the animal is heterozygous for the insertion.

34. The transgenic animal of claim 28, wherein the animal is homozygous for the insertion.

35. The transgenic animal of claim 28, wherein the insertion is in a domain involved in transcriptional activation or in dimerization.

36. The transgenic animal of claim 28, wherein the insertion is in exon 7.

37. The transgenic animal of claim 11, wherein the genome of the animal further comprises an alteration by disrupting at least one exon of the endogenous gene encoding a protein involved in hematopoiesis.

38. The transgenic animal of claim 37, wherein the endogenous gene is disrupted by insertion of a nucleic acid sequence.

39. The transgenic animal of claim 38, wherein the endogenous gene encodes Helios.

40. The transgenic animal of claim 38, wherein the endogenous gene encodes Aiolos.

41. The transgenic animal of claim 38, wherein the insertion results in any of an inversion, deletion, translocation, or reciprocal translocation.

42. A method of evaluating the development of a component or a cell lineage of the immune system, comprising:

providing a transgenic animal of claim 11 or claim 37, or a cell or tissue therefrom; and

monitoring expression of the protein unrelated to Ikaros.

43. The method of claim 42, wherein the sequence functionally unrelated to the Ikaros gene encodes a reporter molecule.

44. The method of claim 43, wherein the reporter molecule is a reporter molecule which can luminesce or fluoresce.

45. The method of claim 43, wherein the sequence encoding the reporter molecule is selected from a beta-galactosidase gene, a luciferase gene, a green fluorescent protein gene, an alkaline phosphatase gene, a horseradish peroxidase gene, and a chloramphenicol acetyl transferase gene.

46. The method of claim 43, wherein the reporter molecule is green fluorescent protein or a variant thereof.

47. The method of claim 46, wherein the reporter molecule is a variant of green fluorescent protein.

48. The method of claim 47, wherein the variant of green fluorescent protein is selected from the group consisting of EGFP, EBFP, EYFP, d2EGFP, ECFP, and GFPuv.

49. The method of claim 43, wherein hematopoietic development is evaluated in a living animal.

50. The method of claim 49, wherein hematopoietic development is evaluated by detecting a fluorescent signal on the live animal.